AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method of performing nanopore data analysis with a nanopore device, comprising:

providing a sample including target polynucleotides and non-target polynucleotides;

introducing the sample to the nanopore device;

generating nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing an aperture of the nanopore;

forming a distribution pattern of the nanopore data points, wherein the distribution pattern includes at least one data cluster; and

analyzing the distribution of target polynucleotide data points within the at least one data cluster; ~~a distribution of polynucleotide data points in the distribution pattern~~

optionally analyzing the distribution of the non-target polynucleotide data points; and determining at least one of the following:

(i) phosphorylation state of the target polynucleotides by comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution,

(ii) length diversity among polynucleotides present in a sample, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides,

(iii) chemical integrity of the target polynucleotides by comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared, and

(iv) a ratio of target polynucleotides to non-target polynucleotides in the sample, ~~and wherein analyzing includes:~~

~~analyzing the distribution of target polynucleotide data points within the at least one data cluster; and~~

~~comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution~~.

2. – 3. (Cancelled)

4. (Currently amended) The method of claim 1, ~~further comprising:~~ wherein said determining comprises

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

5. (Currently amended) The method of claim 1, wherein the target polynucleotides comprise phosphorylated and non-phosphorylated polynucleotides, ~~the method further comprising:~~ wherein said determining comprises

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

6. (Currently amended) The method of claim 1, ~~further comprising:~~ wherein said determining comprises

comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared.

7. (Currently amended) The method of claim 6, ~~further comprising:~~

~~determining~~ wherein the density of target polynucleotide data points in a defined area~~; and~~

~~comparing the density of the target polynucleotide data points~~ is determined and compared to a chemical integrity standard density distribution for the defined area.

8. (Currently amended) The method of claim 6, further comprising:

~~determining the density of target polynucleotide data points in a defined area;~~

comparing the density of the target polynucleotide data points to a density of the target polynucleotide data points of at least two other samples including target polynucleotides and non-target polynucleotides; and

ranking the samples based on the density of the target polynucleotide data points.

9. (Currently amended) The method of claim 6, ~~further comprising:~~ wherein said determining comprises

determining a cluster score for the target polynucleotide data points in a defined area; and

comparing the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area.

10. (Currently amended) The method of claim 1, ~~further comprising:~~ said method comprising

analyzing the distribution of the non-target polynucleotide data points.

11. (Original) The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides.

12. (Cancelled)

13. (Currently amended) The method of claim 10, ~~further comprising:~~ wherein said determining comprises

determining a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

14. (Cancelled)

15. (Currently amended) A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, wherein a polynucleotide traverses the aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing the aperture of the nanopore structure;

form a distribution pattern of the data points; ~~and~~

analyze a distribution of target polynucleotide data points in the distribution pattern; and ~~determining~~

determine at least one of the following:

(i) phosphorylation state of the target polynucleotides, wherein the distribution pattern includes two data clusters and wherein the nanopore data analysis system is operative to:

analyze the distribution of target polynucleotide data points between two data clusters;

compare the distribution of the target polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target polynucleotides to non-phosphorylated target polynucleotides;

(ii) length diversity among polynucleotides present in a sample, wherein the distribution pattern includes at least one data cluster, and wherein the nanopore data analysis system is operative to:

analyze the distribution of non-target polynucleotide data points outside of the at least one cluster that indicates that non-target polynucleotides have a different length than the target polynucleotides

(iii) chemical integrity of the target polynucleotides, wherein the nanopore data analysis system is operative to:

determine a cluster score for the target polynucleotide data points in a defined area; and

compare the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target polynucleotide standard;

and

(iv) a ratio of target polynucleotides to non-target polynucleotides in the sample, wherein the nanopore data analysis system is ~~further~~ operative to analyze the distribution of the non-target data polynucleotide data points~~, wherein the nanopore data analysis system is further operative to determine a ratio between the target polynucleotide data points and the non-target polynucleotide data points~~.

16.-17. (Cancelled)

18. (Currently amended) The system of claim 15, wherein the distribution pattern includes ~~at least one~~ two data ~~cluster~~ clusters and wherein the nanopore data analysis system is ~~further~~ operative to:

analyze ~~of~~ the distribution of target polynucleotide data points between the two data clusters;

compare the distribution of the target polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target polynucleotides to non-phosphorylated target polynucleotides.

19. (Currently amended) The system of claim 15, wherein the nanopore data analysis system is ~~further~~ operative to:

determine a cluster score for the target polynucleotide data points in a defined area; and

compare the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target polynucleotide standard.

20. (Original) The system of claim 15, wherein the nanopore data analysis system is stored on a computer-readable medium.

21. – 35. (Cancelled)

36. (New) The system of claim 15, wherein the nanopore data analysis system is operative to determine a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

37. (New) The system of claim 15, wherein the nanopore data analysis system is operative to determine length diversity among polynucleotides present in a sample.